a.) Amendments to Specification

Please amend the paragraph starting at page 19, line 16 and ending at page 20, line5 to read as follows.

The nucleotide sequence of the 12 Kbp DNA fragment inserted into plasmic pHK162 was determined by the dideoxy method using a DNA sequencer (Pharmacia LKB, ALF DNA Sequencer II). As a result, a gene was found which comprises the region of about 6.5 Kbp cleaved at BamHI (A) and SphI (B) shown in Fig. 1 within the open reading frame. This gene was designated CSF1 gene. As shown in the amino acid sequence of ~~SEQ ID NO: 1~~ SEQ ID NO: 2, the polypeptide encoded by CSF1 gene which is presumed from the determined nucleotide sequence consists of 2958 amino acid residues (molecular weight: 338 kDa). DNA homology search with other genes revealed that the sequence of the upstream region in CSF1 gene comprising about 140 N-terminal amino acid residues in the open reading frame of CSF1 gene coincided with the sequence of the region located upstream of the sequence which was reported as the nucleotide sequence of GAA1 gene of Saccharomyces cerevisiae [Hamburger, et al.: J. Cell Biol., 129, 629-639 (1995)] (the region outside the GAA1 gene-encoding region). However, the report by Hamburger, et al. relates to GAA1 gene and contains no description about the presence of another gene (CSF1 gene) upstream from GAA1 gene. Further, in the nucleotide sequence reported by them, one base (T) is inserted between the base at position 198 (T) and the base at position 199 (G) in the nucleotide sequence of SEQ ID NO: 1. Thus, the polypeptide encoded by CSF1 gene cannot be anticipated from the sequence reported by Hamburger, et al.